UNITED STATES PATENT AND TRADEMARK OFFICE

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

PTOL-90A (Rev. 04/07)

-- *The MAILING DATE of this communication appears on the cover sheet with the correspondence address* --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *27 March 2007*.

2a)☒ This action is **FINAL**.   2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-19* is/are pending in the application.

    4a) Of the above claim(s) *10-18* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-9 and 19* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *27 March 2007* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☐ Notice of References Cited (PTO-892)

2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3)☐ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date _____.

4)☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____.

5)☐ Notice of Informal Patent Application

6)☐ Other: _____.

DETAILED ACTION

Applicant's amendments and remarks, filed 3/27/07, are acknowledged. Amended

claims 1-9 and 19 are acknowledged. Claims 10-18 remain withdrawn from consideration due to

being directed to a non-elected Group.

Applicant's arguments, filed 3/27/07, have been fully considered but they are not deemed

to be persuasive. Rejections and/or objections not reiterated from the previous office actions are

hereby withdrawn. The following rejections and/or objections are either reiterated or newly

applied. They constitute the complete set presently being applied to the instant application.

Claims 1-9 and 19 are herein under examination.

Claim Rejections - 35 USC § 112, First paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making
> and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it
> pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode
> contemplated by the inventor of carrying out his invention.

Claims 2-3, 9, and 19 are rejected under 35 U.S.C. 112, first paragraph, as failing to

comply with the written description requirement. The claim(s) contains subject matter which

was not described in the specification in such a way as to reasonably convey to one skilled in the

relevant art that the inventor(s), at the time the application was filed, had possession of the

claimed invention.

NEW MATTER

Applicant points to written support for the claim amendments on p. 2, lines 9-12; p. 3,

lines 3-4; p. 5, lines 10-13; p. 6, lines 3-5; p. 7, lines 18-19; Table 1 (p. 5); Fig. 4; and claim 3 as

originally filed. There does not appear to be adequate written support for the following phrases:

"a number of base positions that characterize a feature of the extracted difference" (claim 2),

"whether a type of extracted difference occurs in succession in the subject sequence" (claims 2

and 3), "two adjacent variations" (claim 9), and "is not a carrier wave" (claim 19).

While there is written support for "ten numeric characters for 0 through 9" (page 4, line

24 of the specification), this does not provide adequate written support for "a number of base

positions that characterize a feature of the extracted difference" which differs in scope. While

there is written support for "type of the variations" (original claim 9), this does not provide

adequate written support for "whether a type of extracted difference occurs in succession in the

subject sequence" which differs in scope. There does not appear to be any written support for

adjacent variations. Finally, while there is written support for "carrier waves" (page 14, line 19

of the specification), this fails to provide adequate written support for the phrase "is not a carrier

wave". It is noted that negative limitations must have adequate written support in the originally

filed application. Because the introduction of "a number of base positions that characterize a

feature of the extracted difference" (claim 2), "whether a type of extracted difference occurs in

succession in the subject sequence" (claims 2 and 3), "two adjacent variations" (claim 9), and "is

not a carrier wave" (claim 19) do not appear to have adequate written support in the claims,

specification, and/or drawings, as originally filed, these phrases are considered to be NEW

MATTER. This rejection is necessitated by amendment.

Claims Rejected Under 35 U.S.C. § 112, Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9 and 19 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention. These rejections are necessitated by amendment.

Claim 1 recites "a character to represent the extracted difference" which is confusing with respect to the "characters" recited in line 7. The extracted difference is converted into a string of characters in the conversion unit and then a single character represents the extracted difference in the code storage unit. It would seem that either a string or a single character (but not both) would be needed to represent the extracted difference. It is unclear if the "character" in line 10 is only one character from the string of characters or whether the "character" is a different type of character than the stringed characters. A similar issue is present in claims 6 and 19. Clarification of this issue via clearer claim wording is requested. Claims 2-9 are also rejected due to their dependency from claim 1.

Claims 2 (lines 1-2) and 6 (last line) recite the limitation "*the characters* to represent the extracted difference" which is vague and indefinite. Claim 1, from which claims 2 and 6 depend, recites "*a character* to represent the extracted difference" in line 10 which is a single character. However, claims 2 and 6 recite *plural* characters to represent the extracted difference that lacks consistency with what was recited in claim 1. Is it a single character or multiple characters that

represent the extracted difference? Clarification of this issue via clearer claim wording is

requested. Claim 3 is also rejected due to their direct or indirect dependency from claim 2.

Claim Rejections – 35 USC §102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the

basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 6, 7 and 19 are rejected under 35 U.S.C. 102(b) as being anticipated by

Grumbach et al. (Information Processing & Management, Volume 30, Number 6, pages 875-886,

1994). This rejection is maintained and reiterated for reasons of record.

Grumbach et al. disclose using UNIX (computer operating system) and ASCII files with

algorithms to encode DNA sequences (page 876, second and third paragraphs and page 878,

second and third paragraphs) as well as data compression for storage of sequences (page 875,

first paragraph) and compression rates (page 878, fourth paragraph to page 879, second

paragraph) which represents an apparatus and computer readable medium for a encoding DNA

sequence to achieve a high data compression ratio for storage, as stated in the preamble of instant

claims 1 and 19. Grumbach et al. disclose storing a DNA sequence by encoding individual DNA

characters (Figure 1 and page 878, third paragraph). Grumbach et al. disclose using a dictionary

containing already encoded factors (page 879, third paragraph) that represents predetermined

conversion codes. Grumbach et al. disclose having a start position and matching the factor at the current position followed by outputting a codeword (page 881, second paragraph), alignment algorithms working directly on compressed DNA sequences (page 886, first paragraph), compression algorithms including a vertical mode, where a DNA sequence A is compressed with respect to another sequence B with output containing information to construct sequence A from sequence B (page 876, fifth paragraph), using codewords to encode strings and arithmetic encoding (page 876, third paragraph and page 879, first paragraph), and storing a reference sequence in a database while other sequences are stored in a compressed form with respect to it (page 876, fifth paragraph)as well as alignment algorithms working directly on compressed DNA sequences (page 886, first paragraph) which represents the comparative, conversion, code storage, and encoding units (as stated in instant claim 1), the conversion (as stated in instant claim 6), the compression and storage units (as stated in instant claim 7), and the aligning, extracting, converting, and encoding steps (as stated in instant claim 19). Grumbach et al. disclose statistical and substitutional compression of text via encoding blocks of fixed length and encoding factors of different lengths using a pointer to one of their previous occurrences in the text (page 875, third paragraph) which represents a division unit, as stated in instant claim 6. Grumbach et al. disclose using a codeword including "l" for the length of the factor, and "p" for the position of the first occurrence (page 881, first paragraph). Grumbach et al. disclose encoding DNA base symbols on bits of codewords (page 881, last paragraph) and characters representing the number of substitutional difference during compression (page 882, first and second paragraphs). Grumbach et al. disclose using output code containing three types of codewords: literal, numerical, and copy codewords (page 882, first paragraph).

Thus, Grumbach et al. anticipate claims 1, 6, 7, and 19.

Applicant summarizes Grumbach et al. Applicants argue that Grumbach et al. do not disclose

that the apparatus performing either algorithm comprises a comparative unit for aligning a

reference sequence having known DNA information with a subject sequence to be compressed

and extracting a difference between the reference sequence and the subject sequence; a

conversion unit for converting the extracted difference between the reference sequence and the

subject sequence into a string of characters and for outputting the string of characters; a code

storage unit for storing a conversion code that corresponds to a character to represent the

extracted difference; and an encoding unit for encoding the string using the conversion code.

This statement is found unpersuasive as Grumbach et al. disclose UNIX and algorithms (page

876, second and third paragraphs and page 878, second and third paragraphs) and having a start

position and matching the factor at the current position followed by outputting a codeword (page

881, second paragraph), compression algorithms including a vertical mode, where a DNA

sequence A is compressed with respect to another sequence B with output containing

information to construct sequence A from sequence B (page 876, fifth paragraph), using

codewords to encode strings and arithmetic encoding (page 876, third paragraph and page 879,

first paragraph), and storing a reference sequence in a database while other sequences are stored

in a compressed form with respect to it (page 876, fifth paragraph) which represents the

comparative, conversion, code storage, and encoding units (as stated in instant claim 1), the

conversion (as stated in instant claim 6), the compression and storage units (as stated in instant

claim 7), and the aligning, extracting, converting, and encoding steps (as stated in instant claim

19). Applicant argues that Grumbach et al. fail to disclose explicitly in this putative apparatus

comprising UNIX the presence of at least a comparative unit for aligning a reference sequence

having known DNA information with a subject sequence to be compressed and extracting a

difference between the reference sequence and the subject sequence. This statement is found

unpersuasive as Grumbach et al. disclose alignment algorithms working directly on compressed

DNA sequences (page 886, first paragraph) as well as a DNA sequence A is compressed with

respect to another sequence B with output containing information to construct sequence A from

sequence B (page 876, fifth paragraph) wherein the information for construction of A from B

represents extracting a difference in a broad and reasonable interpretation of "extracting a

difference". Applicant summarizes the Biocompress-2 algorithm and argues that Biocompress-2

algorithm is not one of the two compression algorithms available on UNIX (see p. 878, lines 2-3

of"3. Classical Algorithms") and therefore is apparently NOT part of the "apparatus" that the

Examiner alleged is disclosed. This statement is found unpersuasive as Grumbach et al. disclose

using various algorithms (page 876, second paragraph) in addition to compression algorithms

and alignment algorithms working directly on compressed DNA sequences (page 886, first

paragraph). In addition, all of these algorithms inherently take place on a computer. Applicant

argues that Biocompress-2 is disclosed to be based on the "detection and encoding of factors and

palindromes" (p. 876, 3rd paragraph), not on converting an extracted difference between a

reference sequence and a subject sequence into a string of characters as performed by the

conversion unit of claim 1. This statement is found unpersuasive as Grumbach et al. disclose

using genetic-oriented compression algorithms in two compression modes, such as a vertical

mode wherein a DNA sequence A is compressed with respect to another sequence B with output

containing information to construct sequence A from sequence B (page 876, fifth paragraph)

wherein the information for construction of A from B represents extracting a difference in a broad and reasonable interpretation of "extracting a difference" with the output of information as a string of characters. Applicants argue that with respect to the section cited on p. 876, 5th para, disclosing compression algorithms including a vertical mode in which a DNA sequence A is compressed with respect to another sequence B, there is no disclosure of how the vertical mode performs this compression. In particular, there is no disclosure that this vertical mode performs this compression by "aligning a reference sequence having known DNA information with a subject sequence to be compressed and extracting a difference between the reference sequence and the subject sequence". This statement is found unpersuasive as the instant claims do not specifically state that the compression is performed in such a manner. Instant claim 1 (line 4) recites "to be compressed". This phrase is written broadly so that it may mean the subject sequence is compressed or that the alignment is compressed. It is also noted that the "to be compressed" is referring to a future action which may or may not occur in instant claim 1. It is further noted that the apparatus as claimed in claim 1 contains 4 units which are not given further structural limitations, but only intended uses which leads to a very broad interpretation of the claim limitations. Grumbach et al. disclose the use of compression algorithms and alignment algorithms working directly on compressed DNA sequences (page 886, first paragraph) as already mentioned above. Applicant argues the paragraph further states that the output of biocompress-2 contains the information to construct the sequence A from sequence B, but as noted above the Biocompress-2 algorithm is not one of the two compression algorithms available on UNIX (see p. 878, lines 2-3 of paragraph 3. This statement is found unpersuasive Grumbach et al. disclose using the biocompress-2 algorithm (page 885, sixth paragraph) and using

compression algorithms and alignment algorithms directly on compressed sequences (page 886, first paragraph).   It is further noted that all of these algorithms inherently take place on a computer. Applicant argues with respect to the section cited on p. 876, 5th para., disclosing "storing a reference sequence in a database while other sequences are stored in a compressed form with respect to it", this is the only "storing" function noted by the Examiner. This statement is found unpersuasive as the entire reference is used in its entirety to reject claims 1, 6, 7, and 9. Storage is mentioned repeatedly throughout Grumbach et al. including page 875, first paragraph and page 886, first paragraph. Applicant argues that a database with a stored reference sequence and with other sequences stored in compressed form relative to the reference is not equivalent to the recited element, "a code storage unit for storing a conversion code that corresponds to a character to represent the extracted difference". This statement is found unpersuasive as this claim limitation fails to define any physical limitations to a code storage unit besides its intended use. Therefore, anything that is capable of this storage is broadly and reasonably considered to be a code storage unit. Applicant argues that although Grumbach et al. mention use of a dictionary at p. 879, 3rd para., Applicant cannot find in that paragraph any disclosure that the dictionary is for storing a conversion code that corresponds to a character to represent the extracted difference as required by claim 1. This statement is found unpersuasive Grumbach et al. disclose a vertical compression mode wherein a DNA sequence A is compressed with respect to another sequence B with output containing information to construct sequence A from sequence B (page 876, fifth paragraph) wherein the outputted information for construction of A from B represents extracting a difference in a broad and reasonable interpretation of "extracting a difference". Applicant argues thus claims 1, 6, and 7 cannot be anticipated by Grumbach et al.,

as the cited reference fails to disclose each and every element of the claim. This statement is found unpersuasive because Grumbach et al. disclose the limitations of these claims, as described above. Applicant argues that Grumbach et al. are silent with respect to an "extracted difference" between a reference sequence and a subject sequence, consequently, Grumbach et al. fail to disclose a division unit as required by claim 6 and therefore fail to anticipate claim 6. This statement is found unpersuasive as Grumbach et al. disclose a vertical compression mode wherein a DNA sequence A is compressed with respect to another sequence B with output containing information to construct sequence A from sequence B (page 876, fifth paragraph) wherein the information for construction of A from B represents extracting a difference in a broad and reasonable interpretation of "extracting a difference". Grumbach et al. disclose statistical and substitutional compression of text via encoding blocks of fixed length and encoding factors of different lengths using a pointer to one of their previous occurrences in the text (page 875, third paragraph) which represents a division unit, as stated in instant claim 6. Applicant summarizes Grumbach et al. and the instant invention. Applicant argues he cannot find the aligning, extracting, or converting limitations in Grumbach et al. as recited in instant claim 19. This statement is found unpersuasive as Grumbach et al. disclose having a start position and matching the factor at the current position followed by outputting a codeword (page 881, second paragraph), compression algorithms including a vertical mode, where a DNA sequence A is compressed with respect to another sequence B with output containing information to construct sequence A from sequence B (page 876, fifth paragraph), using codewords to encode strings and arithmetic encoding (page 876, third paragraph and page 879, first paragraph), and storing a reference sequence in a database while other sequences are stored

in a compressed form with respect to it (page 876, fifth paragraph)as well as alignment

algorithms working directly on compressed DNA sequences (page 886, first paragraph) which

represents the aligning, extracting, converting, and encoding steps (as stated in instant claim 19).

Applicants argue the "ASCII files with algorithms to encode DNA" on p. 878, 2nd and 3rd para.

alleged by the Examiner to represent the computer readable medium of independent claim 19 do

not have "algorithms" to encode DNA. This statement is found unpersuasive as the UNIX

comprising algorithms run on ASCII files combined in the system used by Grumbach et al.

which represent a medium that is computer readable in a broad and reasonable interpretation of

this limitation.

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-7 and 19 are rejected under 35 U.S.C. 103(a) as being unpatentable over

Grumbach et al. (Information Processing & Management, Volume 30, Number 6, pages 875-886,

1994) in view of Robson et al. (1992). This rejection is maintained and reiterated for reasons of

record.

Grumbach et al. disclose the limitations of instant claims 1, 6, 7, and 19, as discussed in

the 35 USC 102 rejection above. Grumbach et al. describe using characters to code DNA

symbols (page 881, last paragraph) and characters representing the number of substitutional

difference during compression (page 882, first and second paragraphs). Grumbach et al. describe

outputting codewords (page 881, second paragraph). Grumbach et al. do not describe all of the

limitations stated in instant claims 2-5.

Robson et al. describe storing and analyzing nucleic acid sequences including quantifying

and exploring sequence relationships, using standard searching algorithms (i.e. BLAST),

comparing sequences (page 285, column 1, second paragraph and page 288, first paragraph),

encoding sequence information (page 283, first column, last paragraph and second column, third

and fourth paragraphs), assigning code based on a sub-selection defined by classes of properties

(abstract), as well as sorting, searching, and abstracting sub-sets (page 283, col. 2, last

paragraph). Robson et al. describe using 4 bit code (page 286, first column, line 2; page 287,

first column, last paragraph), as stated in instant claim 5. Robson et al. describe using 4 bit codes

which correspond to characters including the start or end of the sequence, continue to read

(occurring in succession), ending, sequence separator (i.e. distance between start and end

position), matches, codes for purines and pyrimidines (i.e. A, G, C), and various other characters

(page 287, column 1, last paragraph to column 2, first paragraph), as stated in instant claims 2

and 3. Robson et al. describe using code to signify differences and their number, such as

unknowns, blanks, and deletions (page 287, first column), as stated in instant claims 2-4.

It would have been obvious to a person of ordinary skill in the art at the time the

invention was made to modify the apparatus of Grumbach et al. by using the 4 bit code words

and characters as taught by Robson et al. where the motivation would have been to perform searching in a more intelligent, structured, and faster manner since numerical bioinformatics descriptions are of value whenever the quality and quantity of information is very large, as stated by Robson et al. (page 284, column 1, third paragraph and abstract).

Thus, Grumbach et al., in view of Robson et al., make obvious claims 1-7 and 19.

Applicant summarizes Robson et al. Applicant argues that Robson et al. do not describe a comparative unit and a code storage unit. This statement is found unpersuasive as these limitations are taught by Grumbach et al. (see 35 USC 102 rejection). Applicant argues that Robson et al. are silent with respect to "a character representing whether a type of extracted difference occurs in succession in the subject sequence". This statement is found unpersuasive for two reasons. First, it is noted that the instant disclosure fails to recite or provide written support for this limitation. Second, the claim language is very broad (i.e. "representing") such that the character does not have to recite this limitation, but broadly and reasonably "represent" it. Robson et al. describe using 4 bit codes which correspond to characters including the start or end of the sequence, continue to read (occurring in succession), ending, sequence separator (i.e. distance between start and end position), matches, codes for purines and pyrimidines (i.e.A, G, C), and various other characters (page 287, column 1, last paragraph to column 2, first paragraph) which represents this limitation. Applicant argues Robson et al. are silent with respect to extracted differences in claims 3, 4, and 5. This statement is found unpersuasive as Grumbach et al. describe this limitation. It is noted that this is a 35 USC 103 rejection, not a 35 USC 102 rejection, such that not all limitations need to come from a single reference. Applicant

again argues about Grumbach et al. failing to describe "extracted difference" which has already

been discussed above and found unpersuasive for the reasons given above.

Claims 1, 6-9, and 19 are rejected under 35 U.S.C. 103(a) as being unpatentable over Grumbach

et al. (Information Processing & Management, Volume 30, Number 6, pages 875-886, 1994) in

view of Selifonov et al. (US 2002/0183934 A1). This rejection is maintained and reiterated for

reasons of record.

Grumbach et al. disclose the limitations of instant claims 1, 6, 7, and 19, as discussed in

the 35 USC 102 rejection above. Grumbach et al. describe using characters to code DNA

symbols (page 881, last paragraph) and characters representing the number of substitutional

difference during compression (page 882, first and second paragraphs). Grumbach et al. describe

outputting codewords (page 881, second paragraph). Grumbach et al. do not describe all of the

limitations stated in instant claims 8 and 9.

Selifonov et al. describe making character strings for polynucleotides (title). Selifonov et

al. describe modifying a parental character string sequence (0025, claim 17) and generating

random variation of sequences via multiplication factors (0075-0076, 0117, 0197), as stated in

instant claim 8. Selifonov et al. describe sequences including lengths, type, number/round of

evolution and nucleic acid shuffling, and mutated fragments of predefined lengths, and software

for sequence string manipulation (0026-0028) as well as mutation types from a parent sequence,

mutation (i.e. single point mutation [total number of variation = 1], continuous mutation over

entire string, triple deletion frameshifts), fragmentation, crossover, ligation, and elitism with string analysis tools (i.e. sequence length, specific substrings) (0075-0080) which represents the variation sequence generation factor, as stated in instant claim 9.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the apparatus of Grumbach et al. by creating a variation sequence as taught by Selifonov et al. wherein the motivation would have been to provide for the rapid evolution of nucleic acids for the generation of encoded molecules (e.g., nucleic acids and proteins) with new and/or improved properties of industrial, agricultural and therapeutic importance which can be created or improved through DNA shuffling procedures, as stated by Selifonov et al. (0008).

Thus, Grumbach et al. in view of Selifonov et al. make obvious claims 1, 6-9, and 19.

Applicant summarizes Selifonov et al. Applicant argues that Selifonov et al. do not describe a comparative unit and a code storage unit. This statement is found unpersuasive as these limitations are taught by Grumbach et al. (see 35 USC 102 rejection). Applicant's arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE

MONTHS from the mailing date of this action. In the event a first reply is filed within TWO

MONTHS of the mailing date of this final action and the advisory action is not mailed until after

the end of the THREE-MONTH shortened statutory period, then the shortened statutory period

will expire on the date the advisory action is mailed, and any extension fee pursuant to 37

CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event,

however, will the statutory period for reply expire later than SIX MONTHS from the date of this

final action.

Papers related to this application may be submitted to Technical Center 1600 by facsimile

transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The

faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG

30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28,

1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is

(571) 273-8300.

Any inquiry concerning this communication or earlier communications from the

examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The

examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Ram Shukla, can be reached on (571) 272-0735.

June 8, 2007

/Carolyn Smith/
Primary Examiner
AU 1631